

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:13:15 ; Search time 30.02 seconds
(without alignments)
340.399 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADRESIHDFCLSVKVVGR.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	501	100.0	92	18 AAW30054	Human placental bi
2	501	100.0	92	21 AAB14166	Human placental bi
3	501	100.0	170	18 AAW30041	Human placental bi
4	501	100.0	170	21 AAB14189	Human placental bi
5	501	100.0	170	21 AAB14190	Human placental bi
6	501	100.0	179	18 AAW30053	Human placental bi
7	501	100.0	179	21 AAB14159	Mature human place
8	501	100.0	197	18 AAW30043	Human placental bi
9	501	100.0	197	21 AAB14160	Human placental bi
10	501	100.0	213	18 AAW30042	Human placental bi
11	501	100.0	213	21 AAB14184	Human placental bi

12	501	100.0	213	21 AAB14200	Human placental bi
13	501	100.0	225	18 AAW30046	Human placental bi
14	501	100.0	225	21 AAB14186	Human placental bi
15	501	100.0	225	21 AAB14201	Human placental bi
16	501	100.0	235	18 AAW30060	Human consensus bi
17	501	100.0	235	21 AAB14167	Human placental bi
18	501	100.0	240	18 AAW30045	Human placental bi
19	501	100.0	240	21 AAB14185	Human placental bi
20	501	100.0	248	18 AAW30044	Human consensus bi
21	501	100.0	248	21 AAB14183	Human placental bi
22	501	100.0	252	18 AAW30040	Human placental bi
23	501	100.0	252	18 AAW13665	Hepatocyte growth
24	501	100.0	252	19 AAW70286	Human tissue facto
25	501	100.0	252	21 AAB14187	Human placental bi
26	501	100.0	259	21 AAB14207	Human placental bi
27	501	100.0	289	21 ABA43821	Human cancer assoc
28	498	99.4	252	22 ABB50286	Kunitz type 2 Ser
29	490	97.8	130	21 AAB14169	Human placental bi
30	488	97.4	130	18 AAW30062	EST R35464 protein
31	472	94.2	153	18 AAW30051	Human placental bi
32	472	94.2	153	21 AAB14161	Human placental bi
33	448	89.4	146	18 AAW30052	Human placental bi
34	448	89.4	146	21 AAB14188	Human placental bi
35	403	80.4	170	18 AAW30061	Human consensus bi
36	403	80.4	179	21 AAB14168	Human placental bi
37	334	66.7	58	18 AAW30047	Human placental bi
38	334	66.7	58	21 AAB14162	Human placental bi
39	297	59.3	51	18 AAW30048	Human placental bi
40	297	59.3	51	21 AAB14163	Human placental bi
41	203	40.5	529	22 AAE09332	Human PRO256 prote
42	203	40.5	529	22 AAB20113	Human immunostimul
43	197	39.3	513	18 AAW27368	Hepatocyte growth
44	197	39.3	513	20 AAW92653	Human HAI-1 protei
45	197	39.3	513	21 AAB19553	Human hepatocyte g

ALIGNMENTS

RESULT 1
AAW30054
ID AAW30054 standard; Protein; 92 AA.
XX
AC AAW30054;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PW WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
DR WPI; 1997-470876/43.

XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Claim 1; Page 67; 110pp; English.
XX
CC The present sequence is a human placental bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 501; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRERSTHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGCGNSNNYLTKECLKK 60
|||||
Db 1 aderslhdfclvskvvgcrasmprrwvynvtdgscqlfvyggcdgnsnnytkeeclick 60

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
|||||
Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92

RESULT 2
AAB14166
ID AAB14166 standard; protein; 92 AA.
XX
AC AAB14166;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human placental bikunin protein fragment # 6.
XX
DE Human; mucociliary dysfunction; mucus; sputum;
XX
KW Chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
OS Homo sapiens.
XX
PN WO200037099-A2.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-GB04381.
XX
XX 22-DEC-1998; 98US-0218913.
PR 17-NOV-1999; 99US-0441966.
XX
XX (FARB) BAYER AG.
XX
XX Hall R, Poll CT, Newton BB, Taylor WJA;

DR WPI; 2000-452127/39.
XX
PT Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
PS Claim 15; Page 90; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
CC are caused by retention and accumulation of mucus. The present sequence
CC consists of residues 1-92 of the mature human placental bikunin
CC protein sequence, which is described in AAB14159.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 501; DB 21; Length 92;
Best Local Similarity 100.0%; Pred. No. 1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRERSIHDFCLVSKVVGRCRASPWWYNVTDGSCQLFVYGGCGNSNNYLTKECLKK 60
|||||
Db 1 adersihdfclvskvvgcrasmprrwvynvtdgscqlfvyggcdgnsnnytkeeclick 60

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
|||||
Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92

RESULT 3
AAB30041
ID AAB30041 standard; Protein; 170 AA.
XX
AC AAB30041;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
KW Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
XX 18-SEP-1997.
XX
XX 10-MAR-1997; 97WO-US03894.
XX
XX 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
XX (FARB) BAYER CORP.
XX
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX

XX WPI; 2000-452127/39.
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT always for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor -
 XX
 XX Claim 14; Page 90; 173pp; English.
 XX Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC a sequence for human placental bikunin protein. This sequence was derived
 CC from a human placental cDNA library by PCR-based amplification. This
 CC protein is a Kunitz-type serine protease inhibitor protein, which can
 CC stimulate the rate of mucociliary clearance of mucus and sputum in lung
 CC airways. Therefore, the present protein may be used for treating lung
 CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
 CC are caused by retention and accumulation of mucus.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 501; DB 21; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.2e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
 Db 1 adersihdfclvskvvgrcrasmprrwvntdgsqqlfvyggcdgnsnnyltkeclkk 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
 RESULT 6
 AAW30053
 ID AAW30053 standard; Protein; 179 AA.
 XX
 AC AAW30053;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE Human placental bikunin.
 XX
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX
 OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 PE 10-MAR-1997; 97WO-US03894.
 XX
 PR 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX

DR WPI; 1997-470876/43.
 XX
 PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 PS Claim 1; Page 67; 110pp; English.
 XX
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 SQ Sequence 179 AA;
 Query Match 100.0%; Score 501; DB 18; Length 179;
 Best Local Similarity 100.0%; Pred. No. 2.4e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRASMPRWYNNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
 Db 1 adersihdfclvskvvgrcrasmprrwvntdgsqqlfvyggcdgnsnnyltkeclkk 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
 RESULT 7
 AAB14159
 ID AAB14159 standard; protein; 179 AA.
 XX
 AC AAB14159;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Mature human placental bikunin protein.
 XX
 KW Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 PN WO200037099-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-GB04381.
 XX
 PR 22-DEC-1998; 98US-0218913.
 PR 17-NOV-1999; 99US-0441966.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Hall R, Poll CT, Newton BB, Taylor WJA;

XX WPI; 2000-452127/39.
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT airways for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor
 XX
 XX Claim 14; Pages 89-90; 173pp; English.
 PS
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC human placental bikunin. This protein is a Kunitz-type serine protease
 CC inhibitor protein, which can stimulate the rate of mucociliary clearance
 CC of mucus and sputum in lung airways. Therefore, the present protein may
 CC be used for treating lung diseases such as CF, CB, BE, and chronic
 CC sinusitis and glue ear which are caused by retention and accumulation of
 CC mucus. The present sequence is the mature human placental bikunin protein
 CC sequence.
 XX
 SQ Sequence 179 AA;
 Query Match 100.0%; Score 501; DB 21; Length 179;
 Best Local Similarity 100.0%; Pred. No. 2.4e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRASPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60
 Db 1 adersihdfclvskvvgrcrasprwvnyntdgsqclfvyygdcgnsnnlytkeecclk 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 61 catvtenatgdlatsrnaadssvpsaprrqds 92
 RESULT 8
 AAW30043
 ID AAW30043 standard; Protein; 197 AA.
 XX
 AC AAW30043;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE Human placental bikunin.
 XX
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor xIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX
 OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 XX 10-MAR-1997; 97WO-US03894.
 XX
 PR 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX
 XX (FARB) BAYER CORP.
 PA
 XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 PI
 XX

DR WPI; 1997-470876/43.
 XX
 XX New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 XX Claim 1; Page 65; 110pp; English.
 PS
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 SQ Sequence 197 AA;
 Query Match 100.0%; Score 501; DB 18; Length 197;
 Best Local Similarity 100.0%; Pred. No. 2.7e-50;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRASPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60
 Db 19 adersihdfclvskvvgrcrasprwvnyntdgsqclfvyygdcgnsnnlytkeecclk 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
 Db 79 catvtenatgdlatsrnaadssvpsaprrqds 110
 RESULT 9
 AAB14160
 ID AAB14160 standard; protein; 197 AA.
 XX
 AC AAB14160;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human placental bikunin mature protein and signal peptide.
 XX
 KW Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Signal_peptide
 FT Protein 19..197
 FT /label= Mature_protein
 XX
 PN WO200037099-A2.
 XX
 XX 29-JUN-2000.
 PD
 XX 22-DEC-1999; 99WO-GB04381.
 PF
 XX

PR 22-DEC-1998; 98US-0218913.
XX 17-NOV-1999; 99US-0441966.
XX (FARB) BAYER AG.
XX PA
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX DR WPI; 2000-452127/39.
XX

XX Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor -
XX

PS Disclosure; Page 162; 173pp; English.

XX Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
CC are caused by retention and accumulation of mucus.
CC Note: the present sequence is defined as SEQ ID 46 in the sequence
CC listing. However, in figure 4E of the specification, SEQ ID 46 is
CC clearly shown as a nucleotide sequence. Therefore, the nucleotide
CC sequence has been described in AAA70393.

XX Sequence 213 AA;

Query Match 100.0%; Score 501; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRESIHDFCLVSKVVGCRASMPRWYNYVTGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 1 adreSIHdfclvskvvgcrasmpRWYnyvtdgscqlfvyggcdgnsnnYltkeclkk 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
DB 61 catvtENatgdlatsrNaadssvpsaprrqds 92

RESULT 12
AAW14200
ID AAB14200 standard; protein; 213 AA.

XX AAB14200;

XX 02-FEB-2001 (first entry)

XX Human placental bikunin protein fragment # 15.

XX Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.

XX Homo sapiens.

XX WO200037099-A2.

XX 29-JUN-2000.

XX 22-DEC-1999; 99WO-GB04381.

XX 22-DEC-1998; 98US-0218913.

PR 17-NOV-1999; 99US-0441966.
XX (FARB) BAYER AG.
XX PA
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX DR WPI; 2000-452127/39.
XX

XX Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor -
XX

PS Claim 13; Page 88; 173pp; English.

XX Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are
CC caused by retention and accumulation of mucus.

XX Sequence 213 AA;

Query Match 100.0%; Score 501; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.9e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADRESIHDFCLVSKVVGCRASMPRWYNYVTGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 1 adreSIHdfclvskvvgcrasmpRWYnyvtdgscqlfvyggcdgnsnnYltkeclkk 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
DB 61 catvtENatgdlatsrNaadssvpsaprrqds 92

RESULT 13
AAW30046
ID AAW30046 standard; Protein; 225 AA.

XX AAW30046;

XX 20-APR-1998 (first entry)

XX Human placental bikunin.

XX Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.

XX Homo sapiens.

XX WO9733996-A2.

XX 18-SEP-1997.

XX 10-MAR-1997; 97WO-US03894.

XX 04-OCT-1996; 96US-0725251.

XX 11-MAR-1996; 96US-0013106.

XX 14-JUN-1996; 96US-0019793.

PA (FARB) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
DR WPI; 2000-452127/39.
XX
PT Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor -
XX
PS Claim 13; Pages 88-89; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are
CC caused by retention and accumulation of mucus.
XX
SQ Sequence 225 AA:

Query Match 100.0%; Score 501; DB 21; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGCRASMPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 adersihdfclvskvvgcrasmprwynvtdgscqlfvyggcdgnsnnyitkeec1kk 60

QY 61 CATVTENATGDIATSRNAADSSVPSAPRRQDS 92
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 catvtenatgdiatsrnaadssvpsaprrqds 92

Search completed: September 10, 2002, 13:17:35
Job time: 260 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:15:15 ; Search time 13.01 Seconds
(without alignments)
172.725 Million cell updates/sec

Title: US-09-218-913D-8
Perfect score: 501

Sequence: 1 ADERSIHDFCLVSKVVGRC.....ATSRNAADSVPSAPRRQDS 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	252	1	US-08-685-660A-7
2	501	100.0	252	2	US-08-974-196-7
3	501	100.0	252	4	US-09-071-709-10
4	501	100.0	252	4	US-09-013-896A-2
5	297	59.3	51	4	US-09-013-896A-10
6	197	39.3	51	4	US-08-685-558A-18
7	192.5	38.4	348	4	US-09-071-709-2
8	180	35.9	58	1	US-08-358-160-71
9	174	34.7	58	3	US-08-676-124-93
10	174	34.7	58	3	US-09-414-878-93
11	174	34.7	58	3	US-09-240-136-93
12	167	33.3	62	1	US-08-358-160-97
13	166	33.1	58	3	US-08-676-124-126
14	166	33.1	58	3	US-09-414-878-126
15	166	33.1	58	3	US-09-240-136-126
16	165	32.9	51	4	US-09-013-896A-28
17	165	32.9	58	3	US-08-676-124-95
18	165	32.9	58	3	US-09-414-878-95
19	165	32.9	58	3	US-09-240-136-95
20	164	32.7	58	1	US-08-463-155A-64
21	164	32.7	58	1	US-08-463-432B-64
22	163	32.5	51	4	US-09-013-896A-11
23	163	32.5	58	1	US-07-664-989B-48
24	163	32.5	58	1	US-08-358-160-1
25	163	32.5	58	1	US-08-463-155A-57
26	163	32.5	58	1	US-08-463-432B-57
27	163	32.5	58	1	US-08-676-125A-23

28 163 32.5 58 1 US-08-676-125A-46 Sequence 46, Appl
29 163 32.5 58 2 US-09-136-012A-23 Sequence 23, Appl
30 163 32.5 58 2 US-09-136-012A-46 Sequence 46, Appl
31 163 32.5 58 3 US-08-676-124-77 Sequence 77, Appl
32 163 32.5 58 3 US-09-414-878-77 Sequence 77, Appl
33 163 32.5 58 3 US-09-240-136-77 Sequence 77, Appl
34 162 32.3 58 1 US-07-664-989B-49 Sequence 49, Appl
35 162 32.3 58 1 US-07-664-989B-51 Sequence 51, Appl
36 162 32.3 58 1 US-08-358-160-24 Sequence 24, Appl
37 162 32.3 58 1 US-08-358-160-26 Sequence 26, Appl
38 162 32.3 58 1 US-08-463-155A-3 Sequence 3, Appl
39 162 32.3 58 1 US-08-463-432B-3 Sequence 3, Appl
40 162 32.3 58 3 US-08-676-124-125 Sequence 125, App
41 162 32.3 58 3 US-09-414-878-125 Sequence 125, App
42 162 32.3 58 3 US-09-240-136-125 Sequence 125, App
43 162 32.3 62 1 US-08-358-160-27 Sequence 27, Appl
44 161 32.1 58 1 US-07-664-989B-87 Sequence 87, Appl
45 161 32.1 58 1 US-08-358-160-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-685-660A-7
; Sequence 7, Application US/08685660A
; Patent No. 5731412
; GENERAL INFORMATION:
; APPLICANT: SHIOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,660A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-685-660A-7

Query Match 100.0% Score 501; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ADERSIHDFCLVSKVVGRCASMPWWNVTDGSQLFVYGGCDGNSNNYUTKECLKK 60

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Db      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTGSCQLFVYGGCDGNSNNYLTKEECLKK 87
QY      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 2
US-09-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,660
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-974-196-7
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Query Match      100.0%; Score 501; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADERSIHDFCLVSKVVGRCRASMPRWYNVTGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTGSCQLFVYGGCDGNSNNYLTKEECLKK 87
QY      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119
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RESULT 3
US-09-071-709-10
; Sequence 10, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
```

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,709
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0513 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-709-10

Query Match      100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADERSIHDFCLVSKVVGRCRASMPRWYNVTGSCQLFVYGGCDGNSNNYLTKEECLKK 60
Db      28 ADERSIHDFCLVSKVVGRCRASMPRWYNVTGSCQLFVYGGCDGNSNNYLTKEECLKK 87
QY      61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db      88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 4
US-09-013-896A-2
; Sequence 2, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/013.896A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1290001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8439
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 252 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-013-896A-2

Query Match 100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDFCLVSKVVGCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVVGCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 87

Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDS 119

RESULT 5
US-09-013-896A-10
; Sequence 10, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-896A-10

Query Match 59.3%; Score 297; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1e-28;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CLVSKVVGCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 61
Db 1 CLVSKVVGCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 51

RESULT 6
US-08-685-558A-18
; Sequence 18, Application US/08685558A
; Patent No. 6225081
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; APPLICANT: MIYAZAWA, Keiji
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685.558A
; FILING DATE: 24-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA Hei 7-187135
; FILING DATE: 24-JUL-1995
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: MKN45
US-08-685-558A-18

Query Match 39.3%; Score 197; DB 4; Length 513;
Best Local Similarity 55.0%; Pred. No. 1.6e-15;
Matches 33; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 5 RSIHDFCLVSKVVGCRASMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKCATV 64
Db 244 KOTEDYCLASNKVGRGSPRWYDPTQICKSFVYGGCLGNKNYDREECILACRGV 303

RESULT 7
US-09-071-709-2
; Sequence 2, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra

;; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,709
;; FILING DATE: Filed Herewith
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CERRONE, MICHAEL C.
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0513 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 348 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BLADNOT04
;; CLONE: 1319265
US-09-071-709-2

Query Match 38.4%; Score 192.5; DB 4; Length 348;
Best Local Similarity 44.0%; Pred. No. 3.4e-15;
Matches 37; Conservative 11; Mismatches 31; Indels 5; Gaps 2;
QY 5 RSHDFCLVSKVVG-RCRASMFRWYNTDGGSCOLFVYGGDGNNSNYLTKEECLKKAT 63
DB 62 KOTEDYCLASNKVGRRCRGSFPRWYDPTQICKSFVYGGCLGNKNYLRREECILACRG 121
QY 64 VTENATGDLATSRNAADSSVPSAP 87
DB 122 V----QGGPLRGSSGAQTPOGP 141

RESULT 8
US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/358,160
;; FILING DATE: 16-DEC-1994
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,031
;; FILING DATE: 13-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/009,319
;; FILING DATE: 26-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/664,989
;; FILING DATE: 01-MAR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: LEY=1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-71

Query Match 35.9%; Score 180; DB 1; Length 58;
Best Local Similarity 52.8%; Pred. No. 1.2e-14;
Matches 28; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 9 DFCLYKVVYGRASMPRWYNTDGGSCOLFVYGGDGNNSNYLTKEECLKKC 61
DB 3 DFCLLPATGTCRAMIPRYYNKSKCEPFYIYGGCGGNANNEKTEECRRTC 55

RESULT 9
US-08-676-124-93
; Sequence 93, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124

;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: PCT/US95/00298
;; FILING DATE: 11-JAN-1995
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: US 08/179,658
;; FILING DATE: 11-JAN-1994
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: US 08/208,265
;; FILING DATE: 10-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: COOPER, IVER P.
;; REGISTRATION NUMBER: 28,005
;; REFERENCE/DOCKET NUMBER: MARKLAND=3B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 93:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-676-124-93

Query Match 34.7%; Score 174; DB 3; Length 58;
Best Local Similarity 49.1%; Pred. No. 6.1e-14;
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 7 IHDFCLVSKVYVGRASMPRWYVNTDSCQLFVYGGCDGNSNNTLTKKECLKKC 61
: ||| ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| :
Db 1 MHSCFAKAEVGPCRASPFRWFNFITRQCEFIYGGCEGQNRFESLECKKMC 55

RESULT 10
US-09-414-878-93
; Sequence 93, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/208,265
;; FILING DATE: 10-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/179,685
;; FILING DATE: 11-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YANKWICH, Leon R
;; REGISTRATION NUMBER: 30,237
;; NAME: ZWICKER, Kenneth P
;; REGISTRATION NUMBER: 43,310
;; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-491-4343
;; TELEFAX: 617-491-8801
;; INFORMATION FOR SEQ ID NO: 93:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 58 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-414-878-93

Query Match 34.7%; Score 174; DB 3; Length 58;
Best Local Similarity 49.1%; Pred. No. 6.1e-14;
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 7 IHDFCLVSKVYVGRASMPRWYVNTDSCQLFVYGGCDGNSNNTLTKKECLKKC 61
: ||| ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| : ||||| ||||| :
Db 1 MHSCFAKAEVGPCRASPFRWFNFITRQCEFIYGGCEGQNRFESLECKKMC 55

RESULT 11
US-09-240-136-93
; Sequence 93, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-93

Query Match 34.7%; Score 174; DB 3; Length 58;
Best Local Similarity 49.1%; Pred. No. 6.1e-14;
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVGRCSRASPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEECLKKC 61
DB 1 MHSFCAKAEVGPGRASFPWFNFTQCEBFYIGCGEGNQNFESLECKKMC 55

RESULT 12

US-08-358-160-97
Sequence 97, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-97

Query Match 33.3%; Score 167; DB 1; Length 62;
Best Local Similarity 52.7%; Pred. No. 4.5e-13;
Matches 29; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVGRCSRASPRWYNYVDGSCQLFVYGGCDGNSNNYLTKEECLKKC 61
DB 1 INGDCPLKVGPGCRARFPFYINSSSKRCKRFYIGCGGNANFNHTLEECRVC 55

RESULT 13

US-08-676-124-126
Sequence 126, Application US/08676124
Patent No. 6010880

GENERAL INFORMATION:
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND-3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-126

Query Match 33.1%; Score 166; DB 3; Length 58;
Best Local Similarity 54.9%; Pred. No. 5.5e-13;
Matches 28; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 11 CLVSKVYVGRCRASPRWYVNTDGSQCLFVYGGCDGNSNNYLTKECLKCC 61
DB 5 CAFFMETGPCRARDRWFNFETGECELFVYGGCGGNSNLFRLRKECKEFC 55

RESULT 14

US-09-414-878-126
Sequence 126, Application US/09414878

Patent No. 6071723

GENERAL INFORMATION:

APPLICANT: DYAX CORP

APPLICANT: MARKLAND, William

APPLICANT: LADNER, Robert C

TITLE OF INVENTION: Inhibitors of Human Plamin Derived

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yankwich & Associates

STREET: 130 Bishop Allen Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02139

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/414,878

FILING DATE: (concurrently herewith)

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/240,136

FILING DATE: 29-JAN-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/676,124

FILING DATE: 07-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/00298

FILING DATE: 11-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/208,265

FILING DATE: 10-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/179,685

FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, Leon R

REGISTRATION NUMBER: 30,237

NAME: ZWICKER, Kenneth P

REGISTRATION NUMBER: 43,310

REFERENCE/DOCKET NUMBER: DYX-007.2P US-2

TELEPHONE: 617-491-4343

TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-414-878-126

Query Match 33.1%; Score 166; DB 3; Length 58;
Best Local Similarity 54.9%; Pred. No. 5.5e-13;
Matches 28; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 11 CLVSKVYVGRCRASPRWYVNTDGSQCLFVYGGCDGNSNNYLTKECLKCC 61
DB 5 CAFFMETGPCRARDRWFNFETGECELFVYGGCGGNSNLFRLRKECKEFC 55

RESULT 15

US-09-240-136-126

Sequence 126, Application US/09240136

Patent No. 6103499

GENERAL INFORMATION:

APPLICANT: DYAX CORP

APPLICANT: MARKLAND, William

APPLICANT: LADNER, Robert C

TITLE OF INVENTION: Inhibitors of Human Plamin Derived

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yankwich & Associates

STREET: 130 Bishop Allen Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02139

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5-inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows 98

SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,136

FILING DATE: (concurrently herewith)

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/676,124

FILING DATE: 07-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/00298

FILING DATE: 11-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/208,265

FILING DATE: 10-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/179,685

FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: YANKWICH, Leon R

REGISTRATION NUMBER: 30,237

NAME: ZWICKER, Kenneth P

REGISTRATION NUMBER: 43,310

REFERENCE/DOCKET NUMBER: DYX-007.2P US-1

TELEPHONE: 617-491-4343

TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-240-136-126

Query Match 33.1%; Score 166; DB 3; Length 58;
Best Local Similarity 54.9%; Pred. No. 5.5e-13;
Matches 28; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:16:05 ; Search time 16.15 Seconds
(without alignments)
547.382 Million cell updates/sec

Title: US-09-218-913D-8
Perfect score: 501
Sequence: 1 ADERSIHDFCLVSKVGRG.....ATSRNAADSSVPSAPRRQDS 92
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	71.9	252	2 JG0185	hepatocyte growth
2	167	33.3	62	2 S07451	proteinase inhibit
3	159	31.7	100	2 A32282	Alzheimer's diseas
4	159	31.7	265	2 A53390	Kunitz-type protei
5	157.5	31.4	765	2 S42880	anyloid precursor-
6	156.5	31.2	484	4 A32761	hypothetical Alzhe
7	156	31.1	64	2 S41399	Kunitz-type protei
8	155.5	31.0	302	1 T1RTGK	tissue factor path
9	155.5	31.0	751	2 A49974	beta-amyloid precu
10	155	30.9	60	1 T1BOR	serum basic protei
11	155	30.9	76	2 S03607	Alzheimer's diseas
12	155	30.9	100	1 T1BOSP	spleen basic prote
13	155	30.9	747	2 JH0773	Alzheimer's diseas
14	155	30.9	770	1 QH0744	Alzheimer's diseas
15	154	30.7	59	2 S00371	isoaprotinin G1 -
16	154	30.7	111	2 S41082	anyloid precursor
17	154	30.7	299	2 I46937	tissue factor path
18	153	30.5	76	2 S04855	Alzheimer's diseas
19	153	30.5	76	2 S06678	Alzheimer's diseas
20	152.5	30.5	300	2 S12143	lipoprotein-associ
21	152.5	30.4	763	2 A49321	anyloid beta (A4)
22	152	30.3	65	1 T1V1VC	venom basic protei
23	150.5	30.0	60	1 T1VRV2	venom basic protei
24	150.5	30.0	122	1 A55115	uterine plasmin/tr
25	150	29.9	110	1 T1T1OR	basic proteinase i
26	150	29.9	396	2 S53325	tissue factor path
27	149	29.7	58	2 S10063	isoaprotinin G2 -
28	149	29.7	61	1 T1V1T1	venom basic protei
29	147	29.3	67	1 T1B0C	trypsin inhibitor,

ALIGNMENTS

RESULT 1

JG0185

hepatocyte growth factor activator inhibitor type 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000

C:Accession: JG0185

R:Itoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.

Biochem. Biophys. Res. Commun. 255, 740-748, 1999

A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz,

A:Reference number: JG0185; MUID:99160423

A:Accession: JG0185

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <ITO>

A:Cross-references: GB:AF099016

C:Superfamily: animal Kunitz-type proteinase inhibitor homology

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 71.9%; Score 360; DB 2; Length 252;

Best Local Similarity 69.6%; Pred. No. 3.6e-31;

Matches 64; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ADERSIHDFCLVSKVGRGCRASMPRWYNTDGSQCLFVYGGCDGNSNYLTKECLKK 60

Db 28 ASRELDVHESGVSKVCKRASIPRWYNITDGSQCFVYGGCGNGNNTQSKKECLDK 87

Oy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDS 92

Db 88 CAGVTENTDDNARNRGADSSVLSVPRKQSA 119

RESULT 2

S07451

proteinase inhibitor 5.II - snake-locks sea anemone

C:Species: Anemonia sulcata (snake-locks sea anemone)

C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-May-1997

C:Accession: S07451; B27222

R:Wunderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1981

A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemoni

A:Reference number: S07451

A:Accession: S07451

A:Molecule type: protein

A:Residues: 1-59 <WUN>

A>Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found

R:Krebs, H.C.; Habermehl, G.G.

Naturwissenschaften 74, 395-396, 1987

A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus de

A:Reference number: A94700

A:Accession: B27222

A:Molecule type: protein

A:Residues: 1-38,'R',40,'B',42,'BB',45-48,'22',51,'2',53-62 <KRE>
C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 33.3%; Score 167; DB 2; Length 62;
Best Local Similarity 52.7%; Pred. No. 4.5e-11;
Matches 29; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 7 IHDCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGCDGNSNNYLTKECLKKC 61
Db 1 INGDCPLKPVGCRAPFRYYNYSKKRCXFIYGGCGGNANFHTLEECKVC 55

RESULT 3
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 13-Aug-1999
C:Accession: A32282
R:Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 158, 908-912, 1989
A:Title: Structure and expression of the alternatively-spliced forms of mRNA for the mou
A:Reference number: A32282; MUID:89149813
A:Accession: A32282
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <YAN>
A:Cross-references: GB:M24397; NID:g200350; PIDN:AAA39929.1; PID:g200351
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing
F:11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 31.7%; Score 159; DB 2; Length 100;
Best Local Similarity 41.9%; Pred. No. 5.3e-10;
Matches 26; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 4 ERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGCDGNSNNYLTKECLKKCAT 63
Db 4 EEVVRVCSEQAETGPCRAMISRWFYDTEGKCVFFYGGCGGNRNFDETCMAVCGS 63

QY 64 VT 65
I:
Db 64 VS 65

RESULT 4
A53390
Kunitz-type proteinase inhibitor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A53390
R:Kramer, K.K.; Duffly, J.Y.; Klemann, S.W.; Bixby, J.A.; Low, B.G.; Pope, W.F.; Roberts,
J. Biol. Chem. 269, 7255-7261, 1994
A:Title: Selective cloning of cDNA for secretory proteins of early embryos. Identificati
A:Reference number: A53390; MUID:94171738
A:Accession: A53390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <KRA>
A:Cross-references: GB:U00165; NID:g501024; PIDN:AAA19108.1; PID:g392040
C:Superfamily: animal Kunitz-type proteinase inhibitor homology
C:Keywords: serine proteinase inhibitor
F:208-258/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 31.7%; Score 159; DB 2; Length 265;
Best Local Similarity 50.0%; Pred. No. 1.4e-09;
Matches 26; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 11 CLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGCDGNSNNYLTKECLKKCA 62

Db 208 CLEPKVTGDCNATMPRYFYNTQTGLCEQFVYTGCEGNGNFFNLEDCMKTCS 259

RESULT 5
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid prec
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein p
A:Reference number: S47528; MUID:94368849
A:Accession: S47528
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing
F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 31.4%; Score 157.5; DB 2; Length 765;
Best Local Similarity 38.5%; Pred. No. 6e-09;
Matches 30; Conservative 17; Mismatches 24; Indels 7; Gaps 3;

QY 1 ADERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGCDGNSNNYLTKEEC 57
I:
Db 300 SKETA-1HDVKAVCSEQAETGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNFSESDYC 358

QY 58 LKKCATV---TENATGDL 72
I:
Db 359 MAVCKTMIPPTPLPTNDV 376

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (

C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted
A:Reference number: A32761; MUID:89346754
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain clo
C:Keywords: cloning artifact

Query Match 31.2%; Score 156.5; DB 4; Length 484;
Best Local Similarity 36.4%; Pred. No. 4.8e-09;
Matches 28; Conservative 14; Mismatches 32; Indels 3; Gaps 1;

QY 4 ERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGCDGNSNNYLTKECLKKCAT 63
I:
Db 205 EEVVRVCSEQAETGPCRAMISRWFYDTEGKCAFFYGGCGGNRNFDETCMAVCGS 264

QY 64 VTENATGDLATSRNAAD 80

[illegible]

Db 340 VIP-----ATAASTPDA 351

RESULT 14

ORHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Contains: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A33260; A33486; I39452; I39451; I39453; I59562; A44
 4668; A28583; A29302; A60803; J00038; S06121; A60335; A59011; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288,'V',365-770 <LEMI>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A:Note: alternative splice form APP(695)
 R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LA>
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; van Duijn, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AA59502.1; PID:g178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
 A:Molecule type: DNA
 A:Residues: 1-530,'QWLMVPVAFWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716,'F',718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AA19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692,'G',694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AA23645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AA23646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-sur
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288,'V',365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascula
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288,'V',365-646,'E',648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756,'S',758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue

EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor protein
A:Reference number: S02638; MUID:88296437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.; *et al.* Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease
A:Reference number: S00707; MUID:88122640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Datta, S.; *et al.* Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor
A:Reference number: S00925; MUID:88122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <P02>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity
A:Reference number: A38949; MUID:88122641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, D.L.; *et al.* Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with Alzheimer's disease
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.; *et al.* Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 653 as Gly
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K. *et al.* Nature 350, 104-107, 1990

Query Match 30.9%; Score 155; DB 1; Length 770;
Best Local Similarity 41.7%; Pred No. 1.1e-08;
Matches 25; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

QY 4 ERSIHDFCLVSVGRCRSMRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKCAT 63
DB 284 EEWVREVCSEQAETGCRAMISRWYFDVTGSKCAFFYGGCGGNRRNFTDEEYCNVAVCGS 343

RESULT 15
S00371
isoaprotinin G1 - bovine hybrid
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Jun-1997
C:Accession: S00371
R:Siemann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H. Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A:Title: Characterization and sequence determination of six aprotinin homologues from sheep
A:Reference number: S00371; MUID:88221840
A:Accession: S00371
A:Molecule type: protein
A:Residues: 1-59 <SIE>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 30.7%; Score 154; DB 2; Length 59;
Best Local Similarity 49.1%; Pred No. 1.1e-09;
Matches 26; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 9 DFCLSVKVVGRCRSMRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKC 61
DB 4 DFCLEPPVTGPKARMIRFYNAKAGLCQPFYVGGCRKSNFNKSAEDCMRTC 56

Search completed: September 10, 2002, 13:18:18
Job time: 133 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:17:56 ; Search time 11.86 seconds
(without alignments)
300.354 Million cell updates/sec

Title: US-09-218-913D-8

Perfect score: 501

Sequence: 1 ADERSIHDFCLVSKVVGRC.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	501	100.0	252	1 SPT2_HUMAN	O43291 homo sapien
2	365	72.9	252	1 SPT2_MOUSE	Q9wu03 mus musculu
3	197	39.3	513	1 SPT1_HUMAN	O43278 homo sapien
4	181	36.1	507	1 SPT1_MOUSE	Q9r097 mus musculu
5	175.5	35.0	69	1 CRPT_BOOMI	P81162 boophilus m
6	170	33.9	58	1 AXPL_ANTA	P81547 anthopleura
7	167	33.3	62	1 IP52_ANESU	P10280 anemonia su
8	166.5	33.2	306	1 TPPI_MOUSE	O54819 mus musculu
9	161	32.1	770	1 A4_RAT	P08592 rattus norv
10	160.5	32.0	751	1 A4_SAISC	Q95241 salmisi sci
11	159	31.7	133	1 EPPI_HUMAN	O95925 homo sapien
12	159	31.7	265	1 TKD1_SHEEP	Q29428 oviv aries
13	159	31.7	770	1 A4_MOUSE	P12023 mus musculu
14	157.5	31.4	765	1 APP2_RAT	P15943 rattus norv
15	156	31.1	64	1 SPT3_HUMAN	P49223 homo sapien
16	156	31.1	87	1 A4_MACFA	P53601 macaca fasc
17	156	31.1	164	1 TKD1_BOVIN	Q28201 bos taurus
18	156	31.1	197	1 MCP1_MELCP	P82968 melithaea c
19	155.5	31.0	302	1 TPPI_RAT	Q02445 rattus norv
20	155	30.9	60	1 IBPS_BOVIN	P00975 bos taurus
21	155	30.9	100	1 BPT2_BOVIN	P04815 bos taurus
22	155	30.9	770	1 A4_HUMAN	P05067 homo sapien
23	154	30.7	300	1 TPPI_RABIT	P19761 oryctolagus
24	153	30.5	76	1 A4_MACMU	P29216 macaca mula
25	152.5	30.4	763	1 APP2_HUMAN	Q06481 homo sapien
26	152	30.3	65	1 IVB3_VIPAA	P00992 vipera amno
27	152	30.3	134	1 EPPI_MOUSE	Q9da01 mus musculu
28	150.5	30.0	60	1 IVB2_DABRU	P00990 dabovia russ
29	150.5	30.0	122	1 UPT1_PIG	Q29100 sus scrofa
30	150	29.9	110	1 IBP_CARCR	P00993 caretta car
31	149	29.7	61	1 IVB1_VIPAA	P00991 vipera amno
32	147	29.3	67	1 IBPC_BOVIN	P00976 bos taurus
33	147	29.3	100	1 BPT1_BOVIN	P00974 bos taurus

34 147 29.3 352 1 AMBP_HUMAN P02760 homo sapien
35 146 29.1 304 1 TPPI_HUMAN P10646 homo sapien
36 146 29.1 352 1 AMBP_BOVIN P00978 bos taurus
37 145 28.9 55 1 ISH2_STOHE P81129 stoichiactis
38 145 28.9 62 1 IVBT_ERIMA P24541 eristocophi
39 144 28.7 346 1 AMBP_MERUN Q62577 meriones un
40 143 28.5 83 1 ELAC_MACEU O62845 macropus eu
41 142 28.3 123 1 IATR_HORSE P04365 equus cabal
42 142 28.3 133 1 EPPI_MACMU Q9bd11 macaca mula
43 142 28.3 3137 1 CA36_CHICK P15989 gallus gall
44 141 28.1 65 1 IVB1_BUNFA P25660 bungarus fa
45 141 28.1 304 1 TPPI_MACMU Q28864 macaca mula

ALIGNMENTS

RESULT 1
SPT2_HUMAN
ID SPT2_HUMAN STANDARD; PRT; 252 AA.
AC O43291; O00271; O14895; Q969E0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
DE activator inhibitor type 2) (HAI-2) (Placental bikunin).
GN SPINT2 OR HAI2 OR KOP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96010584; PubMed=9346890;
RA Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,
RA Kitamura N.;
RT "Purification and cloning of hepatocyte growth factor activator
RT inhibitor type 2, a Kunitz-type serine protease inhibitor.";
RL J. Biol. Chem. 272:27558-27564(1997).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC TISSUE=Placenta;
RX MEDLINE=97277372; PubMed=9115294;
RA Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,
RA Tamburini P.P.;
RT "Identification and cloning of human placental bikunin, a novel serine
RT protease inhibitor containing two kunitz domains.";
RL J. Biol. Chem. 272:12202-12208(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancratic cancer;
RX MEDLINE=98094245; PubMed=9434156;
RA Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,
RA Buechler M., Adler G., Gress T.M.;
RT "Cloning of a new Kunitz-type protease inhibitor with a putative
RT transmembrane domain overexpressed in pancreatic cancer.";
RL Biochim. Biophys. Acta 1395:88-95(1998).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT LEU-200.
RC TISSUE=Colon, and Ovary;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,
CC PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,
CC PROSTATE, TESTIS, THYMUS, AND TRACHEA.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
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CC DR EMBL; AB006534; BAA25024.1; -.
CC DR EMBL; U78095; AAC02781.1; -.
CC DR EMBL; AF027205; AAB84031.1; -.
CC DR EMBL; BC001668; AAH01668.1; -.
CC DR EMBL; BC007705; AAH07705.1; -.
CC DR EMBL; BC011951; AAH11951.1; -.
CC DR EMBL; BC011955; AAH11955.1; -.
CC DR EMBL; BC012868; AAH12868.1; -.
CC DR HSSP; P05067; ITAM.
CC MIM; 605124; -.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW Signal; Polymorphism
FT SIGNAL 1 27
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 200 200 V -> L.
FT CONFLICT 3 3 /FTID-VAR_012482.
FT CONFLICT 11 11 Q -> H (IN REF. 3).
FT CONFLICT 53 53 R -> P (IN REF. 1).
FT CONFLICT 240 240 D -> K (IN REF. 3).
FT CONFLICT 240 240 R -> H (IN REF. 3).
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECAB2B CRC64;

Query Match 100.0%; Score 501; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGVGCRASMPRWYNNVTGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 28 ADERSIHDFCLVSKVGVGCRASMPRWYNNVTGSCQLFVYGGCDGNSNNYLTKECLKK 87
QY 61 CATVTENATGDLATSNRAADSSVPSAPRRQDS 92
DB 88 CATVTENATGDLATSNRAADSSVPSAPRRQDS 119
RESULT 2
SPT2_MOUSE STANDARD; PRT; 252 AA.
AC Q9WU03; Q9WU04; Q9WU05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor
DE activator inhibitor type 2) (HAI-2).
GN SPINT2 OR HAI2.
OS Mus musculus (Mouse).
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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALE/C;
RX MEDLINE=99160423; PubMed=10049781;
RA Itoh H., Kataoka H., Hamasuna R., Kitamura N., Koono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.";
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANTLY EXPRESSED THAN
CC ISOFORM 1.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
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EMBL; AF099016; AAD22172.1; -.
EMBL; AF099019; AAD22173.1; -.
EMBL; AF099020; AAD22174.1; -.
HSSP; P05067; ITAM.
MIM; 605124; -.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF00014; Kunitz_BPTI; 2.
PRINTS; PR00759; BASICPTASE.
SMART; SM00131; KU; 2.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
KW Signal; Alternative splicing.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 37 93 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT VARSPLIC 114 128 PRKQSAEDLSAEIFN -> CFVELSVAALFEYA (IN
FT ISOFORM 3).
FT VARSPLIC 129 252 MISSING (IN ISOFORM 3).
SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;

Query Match 72.9%; Score 365; DB 1; Length 252;
Best Local Similarity 69.6%; Pred. No. 2.6e-33;
Matches 64; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGVGCRASMPRWYNNVTGSCQLFVYGGCDGNSNNYLTKECLKK 60
DB 28 ASRELDVHSCGVSKVGVGCRASIPRWYNNITDGSQCFVYGGCEGNGNYKESCECLK 87
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FT	SIGNAL	1	35
KW	Serine protease inhibitor; Repeat; Glycoprotein; Signal.		

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DR PROSITE; PS01209; LDLRA_1; FALSE_NEG.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 507
FT DOMAIN 244 294
FT DOMAIN 312 348
FT DOMAIN 369 419
FT DISULFID 244 294
FT DISULFID 253 277
FT DISULFID 269 290
FT ACT_SITE 254 255
FT DISULFID 369 419
FT DISULFID 378 402
FT DISULFID 394 415
FT ACT_SITE 379 380
FT CARBOHYD 229 229
FT CARBOHYD 501 501
SQ SEQUENCE 507 AA; 56676 MW; 20CB5DEDCFE46AA7 CRC64;

Query Match
Best Local Similarity 36.1%; Score 181; DB 1; Length 507;
Matches 30; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

* QY 9 DFCLSVKVGRCRASPWWNYVTGSCQLFYVGGDGNNSNNYLTKKECLKKCATV 64
Db 242 DYCLASYKVGRCGSPRWYDPKQICKSFTFGGCLGNKNLYLREEECMLACKDV 297

- RESULT 5
CRPT_BOOMI
ID CRPT_BOOMI STANDARD; PRT; 69 AA.
AC P81162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor carrapatin.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE.
RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
RL Submitted (JAN-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: SERINE-PROTEASE INHIBITOR.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR HSP; P10646; ITFX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT ACT_SITE 18 19
SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match
Best Local Similarity 35.0%; Score 175.5; DB 1; Length 69;
Matches 32; Conservative 8; Mismatches 22; Indels 5; Gaps 2;

QY 9 DF---CLSVKVGRCRASPWWNYVTGSCQLFYVGGDGNNSNNYLTKKECLKKCATV 65
Db 3 DFDKQCVPTADPGCKGFMPWWNYFTSQCEEFYVGGQNDNRYRTKECDKTCAEA- 61

QY 66 ENATGDL 72
Db 62 -SATWDV 67

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RESULT 6
AXPL_ANTAF
ID AXPL_ANTAF STANDARD; PRT; 58 AA.
AC P81547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type proteinase inhibitor AXPI-I.
DE Anthopleura aff. xanthogrammica (Sea anemone).
OS Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinidae; Anthopleura.
OX NCBI_TaxID=152178;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103405; PubMed=9440231;
RA Minagawa S., Ishida M., Shimakura K., Nagashima Y., Shiomi K.;
RT "Isolation and amino acid sequences of two kunitz-type protease
inhibitors from the sea anemone Anthopleura aff. xanthogrammica.";
RL Comp. Biochem. Physiol. 118B:381-386(1997).
CC -!- FUNCTION: SPECIFIC FOR SERINE PROTEASES, ESPECIALLY TRYPSIN. ALSO
WEAK INHIBITION AGAINST ALPHA-CHYMOTRYPSIN, ELASTASE AND SOME
METALLOPROTEASES.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
FT ACT_SITE 17 18
SQ SEQUENCE 58 AA; 6341 MW; DA27216A535EA7CC CRC64;

Query Match
Best Local Similarity 33.9%; Score 170; DB 1; Length 58;
Matches 27; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 7 IHDFCLSVKVGRCRASPWWNYVTGSCQLFYVGGDGNNSNNYLTKKECLKK 61
Db 3 VNEDCLLPKVGPCRAAVPRFYNSDSGRCEGTYGGCHANNFRTKDECKNAC 57

RESULT 7
IP52_ANESU
ID IP52_ANESU STANDARD; PRT; 62 AA.
AC P10280;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease inhibitor 5 II (SA5 II).
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actinidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE OF 1-59.
RA Wunderer G., Machleidt W., Fritz H.;
RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
Anemonia sulcata.";
RL Meth. Enzymol. 80:816-820(1981).
RN [2]
RP SEQUENCE.
RA Krebs H.C., Habermehl G.G.;
RT "Isolation and structural determination of a hemolytic active peptide
from the sea anemone Metridium senile.";
RL Naturwissenschaften 74:395-396(1987).
CC -!- FUNCTION: INHIBITOR OF KALLIKREINS.

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CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
DR PIR: B27222; B27222.
DR PIR: S07451; S07451.
DR HSP: P10646; 1TFX.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
FT DISULFID 5 55 BY SIMILARITY.
FT DISULFID 14 38 BY SIMILARITY.
FT DISULFID 30 51 BY SIMILARITY.
FT ACT_SITE 15 16 REACTIVE BOND (BY SIMILARITY).
FT VARIANT 13 13 P -> R.
FT VARIANT 16 16 A -> G.
FT VARIANT 17 17 R -> G.
FT VARIANT 25 25 S -> L.
FT VARIANT 28 28 K -> R.
FT VARIANT 39 39 G -> R.
SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 33.3%; Score 167; DB 1; Length 62;
Best Local Similarity 52.7%; Pred. No. 4.9e-12;
Matches 29; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 7 IHDFCLSVKVGRCRASPWWNVTDGSCQLFYVGGCDGNSNLYLKECLKKC 61
Db 1 INGDELPKVVGPCRPFPRYYNSSSKRCCKFYGGCGGNANFHTLECEKVC 55

RESULT 8
TFPI_MOUSE
ID TFPI_MOUSE STANDARD; PRT; 306 AA.
AC 054819; Q92208;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (BPI).
GN TFPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=129;
RX MEDLINE=98152575; PubMed=9493581;
RA Chang J.-Y., Monroe D.M., Oliver J.A., Liles D.K., Roberts H.R.;
RT "Cloning, expression, and characterization of mouse tissue factor
RT pathway inhibitor (TFPI).";
RL Thromb. Haemost. 79:306-309(1998).
[2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX MEDLINE=99138770; PubMed=9974373;
RA Chang J.-Y., Monroe D.M., Oliver J.A., Roberts H.R.;
RT "TFPIbeta, a second product from the mouse tissue factor pathway
RT inhibitor (TFPI) gene.";
RL Thromb. Haemost. 81:45-49(1999).
CC -1- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTI-THROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha/TFPIalpha (shown here) and
CC beta/TFPIbeta; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Isoform alpha is expressed in heart and
CC spleen; isoform beta in heart and lung.

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CC -1- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
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CC
CC EMBL; AF004833; AAC40035.1; -.
CC EMBL; AF016313; AAD01586.1; -.
CC HSP: P10646; 1TFX.
CC MGD: MGI:1095418; Tfpi.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF00014; Kunitz_BPTI; 3.
CC PRINTS: PR00759; BASICPTASE.
CC SMART: SM00131; KU; 3.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 3.
CC PROSITE: PS0279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal; Alternative splicing.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 306 TISSUE FACTOR PATHWAY INHIBITOR.
FT DOMAIN 50 100 BPTI/KUNITZ INHIBITOR 1
(VII(A)/TISSUE FACTOR BINDING SITE).
FT DOMAIN 121 171 BPTI/KUNITZ INHIBITOR 2
(FACTOR X(A) BINDING SITE).
FT DOMAIN 225 275 BPTI/KUNITZ INHIBITOR 3.
FT DISULFID 50 100 BY SIMILARITY.
FT DISULFID 59 83 BY SIMILARITY.
FT DISULFID 75 96 BY SIMILARITY.
FT ACT_SITE 60 61 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 121 171 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 146 167 BY SIMILARITY.
FT ACT_SITE 131 132 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 225 275 BY SIMILARITY.
FT DISULFID 234 258 BY SIMILARITY.
FT ACT_SITE 235 271 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 264 264 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPPLIC 218 253 DYRGKPCQLQADGLCKASRRFYNSATGCKHRF -> V
TKEETNGKKNADTYQGFLSSVYHLYFVFRIG (IN
ISOFORM BETA).
FT VARSPPLIC 254 306 MISSING (IN ISOFORM BETA).
FT CONFLICT 68 F -> L (IN REF. 2).
SQ SEQUENCE 306 AA; 34987 MW; D3EA3297E4B6A359 CRC64;

Query Match 33.2%; Score 166.5; DB 1; Length 306;
Best Local Similarity 37.0%; Pred. No. 3.1e-11;
Matches 37; Conservative 9; Mismatches 37; Indels 17; Gaps 2;

QY 9 DFCLSVKVGRCRASPWWNVTDGSCQLFYVGGCDGNSNLYLKECLKKCAT----- 63
Db 119 DFCLEEDPGLCGYMKRYLYNNQTKQCFERFYVGGCLGNRNNFETLDECKKICENPVHSP 178
QY 64 -----VTE-NATGDLATSRNAADSSVPSAPRQD 91
Db 179 SPVNEVQMSDYTDGNTVTDRSTVNNIVVQSPKVPVRRD 218

RESULT 9
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)

```

16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=89312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; X07648; CAA30488.1; -;
DR EMBL; X14066; CAA32229.1; -;
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT BY SIMILARITY.
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT POTENTIAL.
FT DOMAIN 724 770
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345
FT BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
FT CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341
FT BY SIMILARITY.

FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 289 364 E -> V (IN ISOFORM APP(695)).
FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 32.1%; Score 161; DB 1; Length 770;
Best Local Similarity 40.0%; Pred. No. 3.4e-10;
Matches 26; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 4 ERSIHDFCLVWGRCRASPMRWYNTDSCQLFVYGGCDGNSNYLTKECLKKCAT 63
DB 284 EEVREVCEQAETGPCRAMISRWFYDTEGKCAFFYGGCGGNRNFTTEYCMVCGS 343

QY 64 VTENA 68
DB 344 VSSQS 348

RESULT 10
A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; S81024; AAD14347.1; -;
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.


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DR SMART: SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein: Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal: Serine protease inhibitor.
FT SIGNAL 1
FT CHAIN 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 18 751 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 653 695 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT FT 291 341 BY SIMILARITY.
FT FT 300 324 BY SIMILARITY.
FT FT 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 32.0%; Score 160.5; DB 1; Length 751;
Best Local Similarity 37.7%; Pred. No. 3.8e-10;
Matches 29; Conservative 14; Mismatches 31; Indels 3; Gaps 1;

Oy 4 ERSIHDFCLSVKVGCRASPRWYNTDGSQQLFYVGGDGNSSNYLTKEELKKCAT 63
Db 284 EEVREVCSQAETGPCRAMISRWTFDTEGKCAFFYGGGGRNNFDTEYCAVCGS 343
Oy 64 VTENATGDLATSRNAAD 80
Db 344 VIPTTA---ASTPDAVD 357

RESULT 11
EPPI_HUMAN
ID EPPI_HUMAN STANDARD; PRT; 133 AA.
AC O95925; O9HD30; O96SD7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 06-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Epin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN SPINLMI
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE-Epididymis, and Testis;
RX PubMed=11404006;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RA "Cloning and sequencing of human Eppin: a novel family of protease
RA inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP Stavrides G.S., Huckle E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,

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RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
CC -!- PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
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DR EMBL; AF286370; AAC00548.1; -
DR EMBL; AF286369; AAC00547.1; -
DR EMBL; AF286368; AAC00546.1; -
DR EMBL; AL118493; CAB56343.1; -
DR EMBL; AL031663; CAB37635.1; -
DR EMBL; AL031663; CAB36265.1; -
DR HSSP; P00974; 2KAI.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_Bpti; 1.
DR Pfam; PF00095; Wap; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 133 EPPIN.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/KUNITZ INHIBITOR.
FT DISULFID 33 61 BY SIMILARITY.
FT DISULFID 40 65 BY SIMILARITY.
FT DISULFID 48 60 BY SIMILARITY.
FT DISULFID 54 69 BY SIMILARITY.
FT DISULFID 77 127 BY SIMILARITY.
FT DISULFID 86 110 BY SIMILARITY.
FT DISULFID 102 123 BY SIMILARITY.
FT VARSPLIC 1 31 MGSSGLLSLVFLVILLANVQSGITDMLFPR -> MLSKAH
FT SEQUENCE 133 AA; 15284 MW; F7831B203366D9C CRC64;
SQ GCKTALSUG (IN ISOFORM 2).

```

Query Match 31.7%; Score 159; DB 1; Length 133;
Best Local Similarity 47.2%; Pred. No. 8.6e-11;
Matches 25; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Search completed: September 10, 2002, 13:21:45
Job time: 229 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 10, 2002, 13:17:41 ; Search time 25.51 Seconds
(without alignments)
623.894 Million cell updates/sec

Title: US-09-218-913D-8
Perfect score: 501
Sequence: 1 ADERSIHDFCLVSKVVGRC.....ATSRNAADSSVPSAPRRQDS 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaea:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	252	4	Q969E0
2	182	36.3	507	11	Q9D3K4
3	182	36.3	507	11	Q99J04
4	181.5	36.2	984	5	Q9GQK2
5	181.5	36.2	984	5	Q9GQK1
6	177	35.3	59	5	Q9TFP8
7	173	34.5	58	5	Q9TFP9
8	170	33.9	58	5	Q9TFG0
9	170	33.9	195	11	Q9D8Q8
10	169	33.7	154	6	Q9N0X3
11	169	33.7	183	6	Q9N0X5
12	161	32.1	83	13	Q90WA1
13	160.5	32.0	246	11	Q9Z2U8
14	159	31.7	117	4	Q96SD7
15	159	31.7	607	11	Q99K32
16	159	31.7	770	6	Q9TU10

17	158	31.5	351	6	Q9N0X8
18	156.5	31.2	484	4	Q13793
19	156	31.1	63	4	Q96KK2
20	156	31.1	160	11	Q90Z78
21	156	31.1	174	6	Q9N0X2
22	155.5	31.0	132	5	Q9VQF9
23	155.5	31.0	751	11	Q60709
24	155.5	31.0	763	11	Q61482
25	155	30.9	547	4	Q13764
26	155	30.9	747	13	Q91963
27	154	30.7	110	6	Q9N0X4
28	153.5	30.6	3198	5	Q90868
29	152.5	30.4	523	4	Q14594
30	152	30.3	179	6	Q9N0X6
31	151.5	30.2	751	13	Q9DG37
32	151	30.1	83	13	Q90WA0
33	150.5	30.0	3060	5	Q9AV4A
34	150	29.9	137	6	Q9BDL0
35	150	29.9	396	6	Q28874
36	149	29.7	74	11	Q60495
37	148.5	29.6	738	13	Q90W28
38	148	29.5	83	13	Q90W99
39	148	29.5	83	13	Q90W98
40	148	29.5	780	13	Q73683
41	147	29.3	151	4	P78491
42	146	29.1	251	4	Q95103
43	145	28.9	113	5	Q9V508
44	144.5	28.8	2167	5	Q76840
45	144	28.7	169	6	Q9N0X7

ALIGNMENTS

RESULT 1

Q969E0 PRELIMINARY; PRT: 252 AA.
AC Q969E0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY, AND ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012868; AAH12868.1; -
DR EMBL; BC007705; AAH07705.1; -
DR EMBL; BC011951; AAH11951.1; -
DR EMBL; BC011955; AAH11955.1; -
KW Protease.
SQ SEQUENCE 252 AA; 28242 MW; FDD3360C1F3A7057 CRC64;

Query Match 100.0%; Score 501; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.1e-52;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ADERSIHDFCLVSKVVGRCRASMFRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVVGRCRASMFRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKK 87
QY 61 CATVTENATGDLATSRNAADSSVPSAPRQDS 92
Db 88 CATVTENATGDLATSRNAADSSVPSAPRQDS 119

RESULT 2
Q9D3K4 PRELIMINARY: PRT: 507 AA.
AC Q9D3K4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; ICAO.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
DR GlycoProtein; Protease; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56571 MW; 9E0A29B7056D72D CRC64;

Query Match 36.3%; Score 182; DB 11; Length 507;
Best Local Similarity 50.0%; Pred. No. 1.8e-13;
Matches 30; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 5 RSIHDFCLVSKVVGRCRASMFRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKCATV 64
Db 238 KQTEDYCLASYKVGRCGSRFPWYDPKEIQICKSTFTGCGLGKNNYLREECMLACKDV 297

RESULT 3
Q9GQ2 PRELIMINARY: PRT: 507 AA.
AC Q9GQ2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE.
GN PAM.
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Gimmelikhuijzen C.J.P.;
RT "Cloning of peptide alpha-amidating enzymes in Calliactis parasitica.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; IKNT.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonoxxygenase.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.

Query Match 36.3%; Score 182; DB 11; Length 507;
Best Local Similarity 50.0%; Pred. No. 1.8e-13;
Matches 30; Conservative 9; Mismatches 21; Indels 0; Gaps 0;

QY 5 RSIHDFCLVSKVVGRCRASMFRWYNTDGSQCLFVYGGCDGNSNNYLTKEECLKKCATV 64
Db 238 KQTEDYCLASYKVGRCGSRFPWYDPKEIQICKSTFTGCGLGKNNYLREECMLACKDV 297

RESULT 4
Q9GQ2 PRELIMINARY: PRT: 984 AA.
AC Q9GQ2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE.
GN PAM.
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Gimmelikhuijzen C.J.P.;
RT "Cloning of peptide alpha-amidating enzymes in Calliactis parasitica.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; IKNT.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonoxxygenase.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.

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DR SMART; SM00131; KU; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
DR MONOOXYGENASE; Serine protease inhibitor.
KW MONOOXYGENASE 984 AA; 110267 MW; 7AF2D1B74B78EBC CRC64;
SQ SEQUENCE 984 AA; 110267 MW; 7AF2D1B74B78EBC CRC64;

Query Match 36.2%; Score 181.5; DB 5; Length 984;
Best Local Similarity 36.7%; Pred. No. 4.4e-13;
Matches 33; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 2 DRESIHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKKC 61
Db 721 DNKASFPFCMLEHDTGCPRAAMPWFYDFAKARSCTRFYGGCGSNNENFASKRECEAKC 780

QY 62 A-TVTENATGDLATSRNAADSSVPSAPRRQ 90
Db 781 TQIVNSNKKQCKDNGSHISEMTLNNLPSKQ 810

RESULT 5
Q9GQNI O9GQNI PRELIMINARY; PRT; 984 AA.
ID AC O9GQNI; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PEPTIDYLGLYCINE ALPHA-AMIDATING MONOOXYGENASE.
GN PAM.
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN 1
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RT "Cloning of peptide alpha-amidating enzymes in Calliactis
parasitica."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221986; AAC44251.1; .
DR HSP; P12111; 1KNT
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR01258; NHL.
DR InterPro; IPR000720; Pamonooxygenase.
DR Pfam; PF01082; Cu2_monooxygen.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase; Serine protease inhibitor.
SQ SEQUENCE 984 AA; 110266 MW; 4C24E4BCEB3B480D CRC64;

Query Match 36.2%; Score 181.5; DB 5; Length 984;
Best Local Similarity 36.7%; Pred. No. 4.4e-13;
Matches 33; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 2 DRESIHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKKC 61
Db 721 DNKASFPFCMLEHDTGCPRAAMPWFYDFAKARSCTRFYGGCGSNNENFASKRECEAKC 780

QY 62 A-TVTENATGDLATSRNAADSSVPSAPRRQ 90
Db 781 TQIVNSNKKQCKDNGSHISEMTLNNLPSKQ 810

RESULT 6
Q9TWf8 O9TWf8 PRELIMINARY; PRT; 59 AA.
ID AC O9TWf8; 2001 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KALICUDINE 3, ASKC3.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN 1
RP SEQUENCE.
RA MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemare E., Moinier D., Lancelin J.M.,
RA Beress L., Lazdunski M.;
RT "Kalicudines and kaliseptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P31713; 1SHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 59 AA; 6738 MW; 0C7695C3F394D4A5 CRC64;

Query Match 35.3%; Score 177; DB 5; Length 59;
Best Local Similarity 54.5%; Pred. No. 6.2e-14;
Matches 30; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKKC 61
Db 1 INGDELPKVVGRCRAPRPRYYNLSRRCEKFIYGGCGNANPHTLEECEKVC 55

RESULT 7
Q9TWf9 O9TWf9 PRELIMINARY; PRT; 58 AA.
ID AC O9TWf9; 2001 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KALICUDINE 2, ASKC2.
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN 1
RP SEQUENCE.
RA MEDLINE=96027617; PubMed=7559645;
RA Schweitz H., Bruhn T., Guillemare E., Moinier D., Lancelin J.M.,
RA Beress L., Lazdunski M.;
RT "Kalicudines and kaliseptine. Two different classes of sea anemone
toxins for voltage sensitive K+ channels."
RL J. Biol. Chem. 270:25121-25126(1995).
DR HSP; P12111; 2KNT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 58 AA; 6778 MW; F102E71682F1A55C CRC64;

Query Match 34.5%; Score 173; DB 5; Length 58;
Best Local Similarity 52.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 7 IHDFCLVSKVVGRCRASMPRWYVNTDGSQQLFVYGGCDGNSNNYLTKEECLKKC 61

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RESULT 11
Q9NOX5      PRELIMINARY;          PRT;    183 AA.
ID Q9NOX5;
AC AC Q9NOX5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TROPHOBLAST KUNITZ DOMAIN PROTEIN 4.
GN TKDP4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BRED SIMMENTAL X HEREFORD;
RA Green J.A., Maclean J.A. II, Gan X., Xie S., Roberts R.M.;
RT "Cloning and characterization of the expression of trophoblast Kunitz
   domain proteins (TKDP)."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RE EMBl; AF241779; AAF61250.1; -.
DR HSP; P00974; 1BPT.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SK SEQUENCE 183 AA; 20286 MW; BB14492F3971DDB4 CRC64;

Query Match      33.7%; Score 169; DB 6; Length 183;
Best Local Similarity 42.3%; Pred. No. 2e-12;
Matches 33; Conservative 9; Mismatches 28; Indels 8; Gaps 1;

QY 10 FCULSVKVGCRASMPRWNYVTDGSCQLFYGGCDGNSNLYLKKECLKKCAVTENAT 69
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 FCLPVRVTHGSHSSWPYPYNAETGHCEQFTYGLGNGKNFNITEECMKTC----- 165
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 70 GDLATSRNAADSSVPSAP 87
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 166 GGAGSLREHAKSGPOKP 183

RESULT 12
Q9OWA1      PRELIMINARY;          PRT;    83 AA.
ID Q9OWA1;
AC AC Q9OWA1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TEXTILININ.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RT "Plasma inhibitors from the Australian brown snake Pseudonaja
   textilis textilis."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Filippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RE EMBl; AF402324; AAK95519.1; -.
DR SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match      32.0%; Score 160.5; DB 11; Length 246;
Best Local Similarity 36.4%; Pred. No. 3e-11;
Matches 36; Conservative 9; Mismatches 37; Indels 17; Gaps 2;

QY 9 DFCLSVKVGRASMPRWNYVTDGSCQLFYGGCDGNSNLYLKKECLKKCAT----- 63
   ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
Db 112 DFCLEEDPLCGVMKRYLNNTQKGERFVYGGLGNRRNFETLDCKEKICENPVHSP 171
   ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
QY 64 -----VTE-NATGDLSRNRNAADSSVPSAPRQ 90
   ||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
Db 172 SPNVNQMSDYVDGNTVTRSTVNIVVPOSQPKVPRRR 210

RESULT 14
Q96SD7      PRELIMINARY;          PRT;    117 AA.
ID Q96SD7;
AC AC Q96SD7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DJ461P17.2.2 (EPPIIN-2 (WAP-TYPE (WHEY ACIDIC PROTEIN)
   'FOUR-DISULFIDE CORE' DOMAIN AND A KUNITZ/BOVINE PANCREATIC TRYPsin
   INHIBITOR DOMAIN PROTEIN)).
OS Homo sapiens (Human).
GN DJ461P17.2.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
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RA Clark L.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031663; CAC36265.1; -
SQ SEQUENCE 117 AA; 13485 MW; 96161FAB3CFEDB47 CRC64;

Query Match 31.7%; Score 159; DB 4; Length 117;
Best Local Similarity 47.2%; Pred. No. 1.9e-11;
Matches 25; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 9 DFCLVSKVVGRCRASPWWYNTDSCQLFVYGGCDGNSNNYLTKEECLKKC 61
Db 59 DVCEMPKETGCPCLAYFLHWYDKDKNTCSMEFYVGGCGNNNNFQSKANCLNTC 111

RESULT 15

Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
TISSUE;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -
DR HSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF0014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 31.7%; Score 159; DB 11; Length 607;
Best Local Similarity 41.9%; Pred. No. 1.3e-10;
Matches 26; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 4 ERSIHDFCLVSKVVGRCRASPWWYNTDSCQLFVYGGCDGNSNNYLTKEECLKKCAT 63
Db 121 EEVVRVCSEQAETGCRAMISRWYFDVTGKCVPPFYGGCGGNRNNFTDEYCMVACGS 180
QY 64 VT 65
Db 181 VS 182

Search completed: September 10, 2002, 13:21:27
Job time: 226 sec